



NUCLEIC ACID MOLECULES ENCODING RED AND GREEN EMITTING LUCIFERASES

Replacement Sheet
Reply to Office Action
of May 14, 2004

Vadim R. Viviani et al.

Appl. No.: 09/993,874 Atty Docket: SAEG150.01CP1C1

<210> SEQ ID NO 1
<211> LENGTH: 1765
<212> TYPE: DNA
<213> ORGANISM: Phrixothrix vivianii
<220> FEATURE:
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<222> LOCATION: (26)...(1660)

<400> SEQUENCE: 1

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Met Glu Glu Glu Asn Ile Arg His Gly
1 5

gag cgt cct cgt gat ata gtc cat cct ggc tcg gca gga caa caa tta 100
Glu Arg Pro Arg Asp Ile Val His Pro Gly Ser Ala Gly Gln Gln Leu
10 15 20 25

tac caa tca ttg tat aaa ttt gca tct ttt cct gaa gca ata atc gat 148
Tyr Gln Ser Leu Tyr Lys Phe Ala Ser Phe Pro Glu Ala Ile Ile Asp
30 35 40

gct cat aca aat gaa gta ata tca tat gct caa ata ttt gaa acc agc 196
Ala His Thr Asn Glu Val Ile Ser Tyr Ala Gln Ile Phe Glu Thr Ser
45 50 55

tgc cgc tta gct gtt agt ata gaa caa tat ggc ttg aat gaa aac aat 244
Cys Arg Leu Ala Val Ser Ile Glu Gln Tyr Gly Leu Asn Glu Asn Asn
60 65 70

gtt gtg ggt gta tgc agt gaa aac aat ata aac ttt ttt aat cct gtc 292
Val Val Gly Val Cys Ser Glu Asn Asn Ile Asn Phe Phe Asn Pro Val
75 80 85

ctt gct gct tta tac tta gga ata cca gta gca aca tca aat gat atg 340
Leu Ala Ala Leu Tyr Leu Gly Ile Pro Val Ala Thr Ser Asn Asp Met
90 95 100 105

tac aca gat gga gag tta act ggt cat ttg aat ata tca aaa cca act 388
Tyr Thr Asp Gly Glu Leu Thr Gly His Leu Asn Ile Ser Lys Pro Thr
110 115 120

atc atg ttt agt tca aag aaa gca ctc ccg ctt att ctg aga gta cag 436
Ile Met Phe Ser Ser Lys Lys Ala Leu Pro Leu Ile Leu Arg Val Gln
125 130 135

caa aat cta agt ttc att aaa aaa gtc gta gtt atc gat agc atg tac 484
Gln Asn Leu Ser Phe Ile Lys Lys Val Val Val Ile Asp Ser Met Tyr
140 145 150

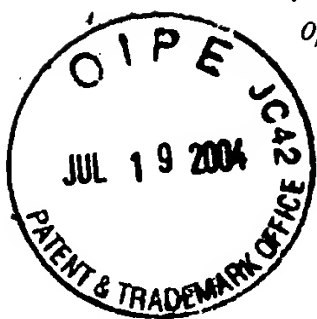
gac att aat ggc gtt gaa tgc gta tct acc ttt gtt gca cgt tat act 532
Asp Ile Asn Gly Val Glu Cys Val Ser Thr Phe Val Ala Arg Tyr Thr

FIG. 1A

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155	160	165	
gac cac acc ttt gat cca ttg tca ttt aca cca aaa gat ttt gat ccc			580
Asp His Thr Phe Asp Pro Leu Ser Phe Thr Pro Lys Asp Phe Asp Pro			
170	175	180	185
ctt gaa aaa atc gca tta att atg tca tca tct gga aca act gga ttg			628
Leu Glu Lys Ile Ala Leu Ile Met Ser Ser Ser Gly Thr Thr Gly Leu			
190	195	200	
cct aag ggt gta gta ctg agc cat aga agt cta act ata aga ttc gtt			676
Pro Lys Gly Val Val Leu Ser His Arg Ser Leu Thr Ile Arg Phe Val			
205	210	215	
cat agc agg gat ccc att tat ggc act cgt acg gtt cca caa aca tca			724
His Ser Arg Asp Pro Ile Tyr Gly Thr Arg Thr Val Pro Gln Thr Ser			
220	225	230	
att ctt tcc tta gta ccg ttc cat cat gcc ttt gga atg ttt act aca			772
Ile Leu Ser Leu Val Pro Phe His His Ala Phe Gly Met Phe Thr Thr			
235	240	245	
tta tct tac ttt gta gta gga ctt aag gtt gta atg ttg aag aaa ttt			820
Leu Ser Tyr Phe Val Val Gly Leu Lys Val Val Met Leu Lys Lys Phe			
250	255	260	265
gag ggc gca ctt ttc tta aaa acc ata cag aat tac aaa atc ccc act			868
Glu Gly Ala Leu Phe Leu Lys Thr Ile Gln Asn Tyr Lys Ile Pro Thr			
270	275	280	
att gta gtg gcc cct cca gtt atg gtg ttt ttg gct aaa agc cca tta			916
Ile Val Val Ala Pro Pro Val Met Val Phe Leu Ala Lys Ser Pro Leu			
285	290	295	
gtc gat caa tac gat tta tgc agc tta acg gaa gtt gct act gga gga			964
Val Asp Gln Tyr Asp Leu Ser Ser Leu Thr Glu Val Ala Thr Gly Gly			
300	305	310	
gct cct tta gga aaa gat gtc gca gaa gca gta gca aag agg ttg aaa			1012
Ala Pro Leu Gly Lys Asp Val Ala Glu Ala Val Ala Lys Arg Leu Lys			
315	320	325	
tta cct gga atc ata caa gga tat gga tta act gaa act tgc tgc gct			1060
Leu Pro Gly Ile Ile Gln Gly Tyr Gly Leu Thr Glu Thr Cys Cys Ala			
330	335	340	345
gta atg att acc cct cat aat gct gtg aaa aca ggt tca act gga aga			1108
Val Met Ile Thr Pro His Asn Ala Val Lys Thr Gly Ser Thr Gly Arg			
350	355	360	
ccc ttg cca tac att aaa gct aaa gtt tta gat aac gct act ggg aag			1156
Pro Leu Pro Tyr Ile Lys Ala Lys Val Leu Asp Asn Ala Thr Gly Lys			
365	370	375	
gcg cta gga cca gga gaa aga ggc gaa ata tgc ttt caa agt gaa atg			1204
Ala Leu Gly Pro Gly Glu Arg Gly Glu Ile Cys Phe Gln Ser Glu Met			
380	385	390	
att atg aaa gga tat tac aac aat ccg gaa gca act att gat act att			1252
Ile Met Lys Gly Tyr Tyr Asn Asn Pro Glu Ala Thr Ile Asp Thr Ile			
395	400	405	
gac aaa gat ggt tgg ctt cat tct gga gat att gga tat tac gac gaa			1300
Asp Lys Asp Gly Trp Leu His Ser Gly Asp Ile Gly Tyr Tyr Asp Glu			
410	415	420	425
gat gga aat ttc ttt ata gtt gat cga ttg aaa gaa ctt att aaa tac			1348
Asp Gly Asn Phe Phe Ile Val Asp Arg Leu Lys Glu Leu Ile Lys Tyr			
430	435	440	
aag gga tat cag gtt gcg cct gct gaa ctg gaa aat ctg ctt tta caa			1396
Lys Gly Tyr Gln Val Ala Pro Ala Glu Leu Glu Asn Leu Leu Leu Gln			
445	450	455	
cat cca agt att gct gat gcg ggt gtt act gga gtt ccg gac gaa ttt			1444
His Pro Ser Ile Ala Asp Ala Gly Val Thr Gly Val Pro Asp Glu Phe			

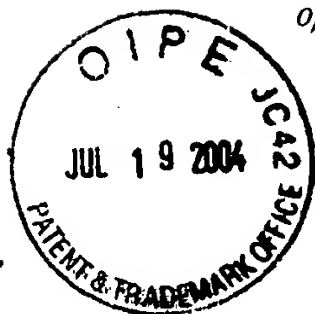
FIG. 1B

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460	465	470	
ggt gga caa tta cct gct gct tgt gtt gtg tta gaa tct ggc aag acg			1492
Gly Gly Gln Leu Pro Ala Ala Cys Val Val Leu Glu Ser Gly Lys Thr			
475	480	485	
ctg act gaa aag gaa gtt caa gat ttt att gca gca caa gtc act cca			1540
Leu Thr Glu Lys Glu Val Gln Asp Phe Ile Ala Ala Gln Val Thr Pro			
490	495	500	505
aca aag cat ctt cga ggc ggt gtc gta ttt gta gac agt att ccg aaa			1588
Thr Lys His Leu Arg Gly Gly Val Val Phe Val Asp Ser Ile Pro Lys			
510	515	520	
ggc cct act gga aaa ctc atc aga aag gag ctc cga gaa ata ttt gcc			1636
Gly Pro Thr Gly Lys Leu Ile Arg Lys Glu Leu Arg Glu Ile Phe Ala			
525	530	535	
cag cga gca cca aaa tca aaa tta taagttcaat gtattgcttt agttctaaaa			1690
Gln Arg Ala Pro Lys Ser Lys Leu			
540	545		
tgtatataaa caagtttttag aacctaatac attcattcaa atactaaaca aaaaaaaaaa			1750
aaaaaaaaaa aaaaa			1765

FIG. 1C